n/a

1641 1802

**CRF Errors Corrected by the STIC System Branch**

CRF Processing Date: 9/9/98

**Serial Number:** 08/876,732

Edited by: _____

Verified by: _____ (STIC staff)

RECEIVED

APR 26 2000

ENTERED

TECH CENTER 1600/2900

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

**RAW SEQUENCE LISTING**
PATENT APPLICATION *US/08/876,132*

DATE: 04/28/00
TIME: 10:17:14

*INPUT SET: S28494.raw*

**This Raw Listing contains the General Information Section and up to the first 5 pages.**



SEQUENCE LISTING

(1) General Information

(i) APPLICANT: Fowler, Timothy
Stuart, Causey

(ii) TITLE OF THE INVENTION: ENTEROBACTERIACEAE FERMENTATION STAINS

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genencor International, Inc.
(B) STREET: 925 Page Mill Road
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 94304-1013

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/876,132
(B) FILING DATE: 23-JUN-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Glaister, Debra J.
(B) REGISTRATION NUMBER: 33,888
(C) REFERENCE/DOCKET NUMBER: GC372

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-846-7620
(B) TELEFAX: 650-845-6504

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1660 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGATCTACAC AAGGCAAATT GAAAAAATAG ATAAAATTTT CGCAGGTATT AAAGCCGACT 60
TAAAACAAAT GAGTGAAGAA GAAAAGAAAA AAATAAATAC ATATTTTGAG TTAGTAAAAG 120
AGAAAGAAAA AATAAAAGAA GACCTCGGCT TAACAGTCGA AAAACCAGAA ATAATAAAAA 180
GAAAGAGACT GTGATTTTTA ATGGAAATCG TGAGGAAAAG AAAATTTTAA TTTTCATTTT 240
CGAGGGATTA ATTTGTTGTA AGTTGATGAA AAATCTAGAT AAAAAATGCA GATCAAAAAT 300
GTGTTGAATT TGACATTATT GAAATACGTA GTATATCAAT AATGGGGGTT TGTCTATTTT 360
ATTTTGCGAA GATTGAAAAT CTGAGTGAAA GAAAATAGTT TGCGAGAGCA AAAAAACCCT 420
TGCCGTTTTT TTCAAATGAC TTTGGAAAAA ATTCATTGTG AGCGGTAGCG AAACTTTGAA 480
ATTTTTTACA TTGGAAATTT GAAAAAATAA GGCAAAAGAA ACTCAAATGG AAAAAATATT 540
ATTATAAAAA AAGGAGATCG GATATGGATT TTAAAAGCAG AAAACTGACA TTGAATGAAA 600
AAAAAGATTT GGAAAAAATC TATGCTGAGA GTGAATTAAA AGCAAAAAAA TTGGGAACTC 660
AACCCGGTGT TGTTTTAGAA ATGACGATGA AAGAAATGAT GAAAAATATC AACCTCGATG 720
TTAATGAAGA AACAGCAGGT CAATATAGGA AATTATTCAA AAATAAAGTT GAGCATAGTA 780
AATCAGATGA TCTAGTAACG GGACTATTAG AGTGTGGAAC TCGAAATAGT TTTGATAAAA 840
CAAGAAGTGC CTTTCGTTTT TGTATTTGTG AGAGAATTCA GCAACTGAGA AAAGAAGCTG 900
ATAATGCAAG AAGAGTAAAA GATTTCGATA CAATGAAAGC AAAAACTAAA GAGGCTTTTG 960
AATTGAGTTT TGTTTTTGAT AAGGATTTTT TGAGTGAAAA TAGAATTCAA TGGAATGATA 1020
TTTCTCACAA CAAAAAAGAC TCTGCAAGTA AAAGAAAAAC AATGAAAGAA GCGGACACAA 1080
TGGATGATAT TTTTAAGAGG CTAAAAAATA ATAAATCTAC ATATGATCGT TATGCTGGAT 1140
TCCTTTCTAT TTGTTCGATT ACAGGTTGCA GACCAGCAGA AGTTTTAAAG GGTATAGAGA 1200
TAGTAAGAAA CAGATATGAG GATGGTATAT CTTTTAAAAT ACTTGGTGCA AAGGTTGGAA 1260
ATGACAGAGG GCAAAGCGAA AGAACATTAC ATTTTGATTT ATCAAAATAT CATGATAATG 1320
AGCAAATGAA TTATATTTTG TCGCAATTAA AAGATAATAA ATTTTTCTAC AAACCAGATG 1380
GGAAGCTCTA CAACAGCTTG AGGCAATACC TCTACATCCA ACATAGAACG TTTTCACTGT 1440
ATACACTTCG TCACAGGGTT GCGAGTGATC TCAAGGCATC CGGTGCAGAT GACTTCACCA 1500
TAGCGGCTNT TTTGGGTCAC AGAGTGACTC AAAGCCAGGA GTTACTACGG CTATGCTCGT 1560
TCGTCGNAAG GTGGTATCGC TGTAACTGGT GTTGAGTGCT CTGATGTTGT GAAAGCAAAC 1620
AAGAGTCAGT TNGCTGTATC AAGGACTCCG AGCCAGATCT 1660

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1847 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGATCTCAAC CAGTTTAAAA TCGCACTTCA AGAAGTAAAA ATAGGGGCCG GCACCGGCTC 60
TTTTTTTGGT GTTTTTGTAG TTAGTGGATA TATCTGTTAG CTACAGAGAA AAGCGATTTT 120
AGAGGGTTTG ACGAGGTTTT TTCGAGCTAT CCAGGGTTTT TGGGTTTTTG GGGTTGGATC 180
AGAAAAGTCG TTCAAGATTA TTGACATAAA GACAGGAAGG TTTATAACAA GTACCAGATA 240
CGACAAAACC AGCTTTGCAG GCTGGCTTTG AAGGACTAAA AGAAGTGGGG ACTTCTTTGA 300

GTCTTGTAAT CAAGTTGGTC AGAACTCGAT TACGATTTGT AAGTAGAAAT CTAACTCACA 360
TTTCGCAGAA AGTCAAACTT ACCTCTTAGT TACAACTCAA AAATTTCCTA GCCTTTTCAG 420
ATCCTTAAGC ATACATATTT TGTTTAAACC GATTGTGTCC GGTGTTTGGT GTGGAGCCAT 480
TGATCCGAGT GGTCAATATG TGATTGTTCG CCAAACAGTG TATGTAGGTC TAAACGGGGA 540
GTGCTACAAA AGACCATACC CGAAACGAGT GCCTAAGTGT TTTGGTTATC AACCAGGTAA 600
GCTATGAGAA AGCCCAGCCA TAAATGGGGT TAGGTTGAAG CAAGTCTTCA TATGGTGCGA 660
CACAAGGGGT GTAGTAGGGT GTCGTCAAAC TGAAAGGTTT GATAGCTCTA AGCTTGTGCT 720
TCTGTGGGTC AAGCCTCAAG TGCTGATCTG TGGTGTCGTC TACCTGATAA CTTTCACTTT 780
TTCGAGTGAA ATTCAGGAGG CGAAACTATG GGTCAAGCCC AGCTTTGCTG GGGTTCGGCA 840
CATCCAGCTT ACAGCATTGG TGCTCTTGCG AAGCTGAAGC ACAAAAATCT AATCCAGGGT 900
TTGGGTTTTT TATACCAGAA GCAAAACAAA AAAATAAAAC AAAGAAAAAT TTTCGAGCGA 960
AAAAATATTT TGGAATTTTT TAAAGGCGAT ACTTGCTACC GCACTTTTGC CATATTTAAA 1020
ACCTGACTAT CTTTATAAGT TAATAGATAT ATCCGTTAGA TTATAAAGTA TGTTAAAAAC 1080
GAGTAAAAAC AATAACTTAT ATATTTAATT CTGAATTATA TTTGACAGTG ATTATTTAAT 1140
ATATTAAGAG ATATATCTAT TAGCTTAAAT ATAACTAAAA AAAGAGGTAA ATATATGGAT 1200
TGTGTATTTA AAAAAGCATT AGAAAATGAA ATAGAACATT ATAAAAAAGA CGGTGATATC 1260
AAATCTTTCT TACAATACTT GCATTACTTT GATATAGATA AAGCATTAAA TGGTGATGAA 1320
TGTGGCGATA TTATAAACTC AAATTTATCC ATTGATGAAA GTTTTGATCT TCTTGATGTT 1380
GAGCACAATT TCGGCTGGGC TTTCAATAAA ATAATACAGA GACGAAATGA ATATTTATCA 1440
TCAGCTAAAA CTGAAAATGA TTTTAAAAAA TACTCGTTCT TTATTCATTC GATCAATTGG 1500
GAAGAATTTA ATTACGATGA GATGAGTACA ATACATCAAG AAATGATTAA AGGATTAGAT 1560
AATTACACAT ATGGAGAAAT AACCATATGA ATAATAAAAT AAGAGAATAT ATTGATTTCG 1620
AAATAACAAA AGATATAAAA GAAAGTCAGC TCTTAAAAAT ATCTGCATTG ATCGATGTTT 1680
TAAAAGTAGA TGAAAAATTT ATTGATGAAG AGGATTTGCA ACTAAAGATA TTGAAAATAT 1740
CGTATGAAAA TCCTATTGAT GATCCAGATG ATGGCATAAG AAAATCACAA TTCGCACGAA 1800
GAAATGCCTA TGCTTTCCGC ATTAAAAAAA CAAGCAAAAA GAGATCT 1847

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Asn Phe Leu His Trp Lys Phe Glu Lys Ile Arg Gln Lys Lys Leu Lys
 1               5                  10                  15

Trp Lys Lys Tyr Tyr Tyr Lys Lys Arg Arg Ser Asp Met Asp Phe Lys
            20                  25                  30

Ser Arg Lys Leu Thr Leu Asn Glu Lys Lys Asp Leu Glu Lys Ile Tyr
        35                  40                  45

Ala Glu Ser Glu Leu Lys Ala Lys Lys Leu Gly Thr Gln Pro Gly Val
    50                  55                  60

Val Leu Glu Met Thr Met Lys Glu Met Met Lys Asn Ile Asn Leu Asp
65                  70                  75                  80

Val Asn Glu Glu Thr Ala Gly Gln Tyr Arg Lys Leu Phe Lys Asn Lys
```

```
                    85                  90                  95

Val Glu His Ser Lys Ser Asp Asp Leu Val Thr Gly Leu Leu Glu Cys
            100                 105                 110

Gly Thr Arg Asn Ser Phe Asp Lys Thr Arg Ser Ala Phe Arg Phe Cys
        115                 120                 125

Ile Cys Glu Arg Ile Gln Gln Leu Arg Lys Glu Ala Asp Asn Ala Arg
    130                 135                 140

Arg Val Lys Asp Phe Asp Thr Met Lys Ala Lys Thr Lys Glu Ala Phe
145                 150                 155                 160

Glu Leu Ser Phe Val Phe Asp Lys Asp Phe Leu Ser Glu Asn Arg Ile
                165                 170                 175

Gln Trp Asn Asp Ile Ser His Asn Lys Lys Asp Ser Ala Ser Lys Arg
            180                 185                 190

Lys Thr Met Lys Glu Ala Asp Thr Met Asp Asp Ile Phe Lys Arg Leu
        195                 200                 205

Lys Asn Asn Lys Ser Thr Tyr Asp Arg Tyr Ala Gly Phe Leu Ser Ile
    210                 215                 220

Cys Ser Ile Thr Gly Cys Arg Pro Ala Glu Val Leu Lys Gly Ile Glu
225                 230                 235                 240

Ile Val Arg Asn Arg Tyr Glu Asp Gly Ile Ser Phe Lys Ile Leu Gly
                245                 250                 255
Ala Lys Val Gly Asn Asp Arg Gly Gln Ser Glu Arg Thr Leu His Phe
            260                 265                 270

Asp Leu Ser Lys Tyr His Asp Asn Glu Gln Met Asn Tyr Ile Leu Ser
        275                 280                 285

Gln Leu Lys Asp Asn Lys Phe Phe Tyr Lys Pro Asp Gly Lys Leu Tyr
    290                 295                 300

Asn Ser Leu Arg Gln Tyr Leu Tyr Ile Gln His Arg Thr Phe Ser Leu
305                 310                 315                 320

Tyr Thr Leu Arg His Arg Val Ala Ser Asp Leu Lys Ala Ser Gly Ala
                325                 330                 335

Asp Asp Phe Thr Ile Ala Ala Xaa Leu Gly His Arg Val Thr Gln Ser
            340                 345                 350

Gln Glu Leu Leu Arg Leu Cys Ser Phe Val Xaa Arg Trp Tyr Arg Cys
        355                 360                 365

Asn Trp Cys
```

206 370
207
208
209

**SEQUENCE VERIFICATION REPORT**
PATENT APPLICATION *US/08/876,132*

DATE: 09/16/98
TIME: 10:17:20

***INPUT SET: S28494.raw***

| Line | Error | Original Text |
|---|---|---|

**RAW SEQUENCE LISTING**
PATENT APPLICATION *US/08/876,132*



*INPUT SET: S28494.raw*

**This Raw Listing contains the General Information Section and up to the first 5 pages.**

SEQUENCE LISTING

(1) General Information

Does Not Comply
Corrected Diskette Needed

(i) APPLICANT: Fowler, Timothy
Stuart, Causey

(ii) TITLE OF THE INVENTION: ENTEROBACTERIACEAE FERMENTATION STAINS

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genencor International, Inc.
(B) STREET: 925 Page Mill Road
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 94304-1013

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/876,132
(B) FILING DATE: 23-JUN-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Glaister, Debra J.
(B) REGISTRATION NUMBER: 33,888
(C) REFERENCE/DOCKET NUMBER: GC372

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-846-7620
(B) TELEFAX: 650-845-6504

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1660 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGATCTACAC AAGGCAAATT GAAAAAATAG ATAAAATTTT CGCAGGTATT AAAGCCGACT 60
TAAAACAAAT GAGTGAAGAA GAAAAGAAAA AAATAAATAC ATATTTTGAG TTAGTAAAAG 120
AGAAAGAAAA AATAAAAGAA GACCTCGGCT TAACAGTCGA AAAACCAGAA ATAATAAAAA 180
GAAAGAGACT GTGATTTTTA ATGGAAATCG TGAGGAAAAG AAAATTTTAA TTTTCATTTT 240
CGAGGGATTA ATTTGTTGTA AGTTGATGAA AAATCTAGAT AAAAAATGCA GATCAAAAAT 300
GTGTTGAATT TGACATTATT GAAATACGTA GTATATCAAT AATGGGGGTT TGTCTATTTT 360
ATTTTGCGAA GATTGAAAAT CTGAGTGAAA GAAAATAGTT TGCGAGAGCA AAAAAACCCT 420
TGCCGTTTTT TTCAAATGAC TTTGGAAAAA ATTCATTGTG AGCGGTAGCG AAACTTTGAA 480
ATTTTTTACA TTGGAAATTT GAAAAAATAA GGCAAAAGAA ACTCAAATGG AAAAAATATT 540
ATTATAAAAA AAGGAGATCG GATATGGATT TTAAAAGCAG AAAACTGACA TTGAATGAAA 600
AAAAAGATTT GGAAAAAATC TATGCTGAGA GTGAATTAAA AGCAAAAAAA TTGGGAACTC 660
AACCCGGTGT TGTTTTAGAA ATGACGATGA AAGAAATGAT GAAAAATATC AACCTCGATG 720
TTAATGAAGA AACAGCAGGT CAATATAGGA AATTATTCAA AAATAAAGTT GAGCATAGTA 780
AATCAGATGA TCTAGTAACG GGACTATTAG AGTGTGGAAC TCGAAATAGT TTTGATAAAA 840
CAAGAAGTGC CTTTCGTTTT TGTATTTGTG AGAGAATTCA GCAACTGAGA AAAGAAGCTG 900
ATAATGCAAG AAGAGTAAAA GATTTCGATA CAATGAAAGC AAAAACTAAA GAGGCTTTTG 960
AATTGAGTTT TGTTTTTGAT AAGGATTTTT TGAGTGAAAA TAGAATTCAA TGGAATGATA 1020
TTTCTCACAA CAAAAAAGAC TCTGCAAGTA AAAGAAAAAC AATGAAAGAA GCGGACACAA 1080
TGGATGATAT TTTTAAGAGG CTAAAAAATA ATAAATCTAC ATATGATCGT TATGCTGGAT 1140
TCCTTTCTAT TTGTTCGATT ACAGGTTGCA GACCAGCAGA AGTTTTAAAG GGTATAGAGA 1200
TAGTAAGAAA CAGATATGAG GATGGTATAT CTTTTAAAAT ACTTGGTGCA AAGGTTGGAA 1260
ATGACAGAGG GCAAAGCGAA AGAACATTAC ATTTTGATTT ATCAAAATAT CATGATAATG 1320
AGCAAATGAA TTATATTTTG TCGCAATTAA AAGATAATAA ATTTTTCTAC AAACCAGATG 1380
GGAAGCTCTA CAACAGCTTG AGGCAATACC TCTACATCCA ACATAGAACG TTTTCACTGT 1440
ATACACTTCG TCACAGGGTT GCGAGTGATC TCAAGGCATC CGGTGCAGAT GACTTCACCA 1500
TAGCGGCTNT TTTGGGTCAC AGAGTGACTC AAAGCCAGGA GTTACTACGG CTATGCTCGT 1560
TCGTCGNAAG GTGGTATCGC TGTAACTGGT GTTGAGTGCT CTGATGTTGT GAAAGCAAAC 1620
AAGAGTCAGT TNGCTGTATC AAGGACTCCG AGCCAGATCT 1660

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1847 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGATCTCAAC CAGTTTAAAA TCGCACTTCA AGAAGTAAAA ATAGGGGCCG GCACCGGCTC 60
TTTTTTTGGT GTTTTTGTAG TTAGTGGATA TATCTGTTAG CTACAGAGAA AAGCGATTTT 120
AGAGGGTTTG ACGAGGTTTT TTCGAGCTAT CCAGGGTTTT TGGGTTTTTG GGGTTGGATC 180
AGAAAAGTCG TTCAAGATTA TTGACATAAA GACAGGAAGG TTTATAACAA GTACCAGATA 240
CGACAAAACC AGCTTTGCAG GCTGGCTTTG AAGGACTAAA AGAAGTGGGG ACTTCTTTGA 300

```
GTCTTGTAAT CAAGTTGGTC AGAACTCGAT TACGATTTGT AAGTAGAAAT CTAACTCACA    360
TTTCGCAGAA AGTCAAACTT ACCTCTTAGT TACAACTCAA AAATTTCCTA GCCTTTTCAG    420
ATCCTTAAGC ATACATATTT TGTTTAAACC GATTGTGTCC GGTGTTTGGT GTGGAGCCAT    480
TGATCCGAGT GGTCAATATG TGATTGTTCG CCAAACAGTG TATGTAGGTC TAAACGGGGA    540
GTGCTACAAA AGACCATACC CGAAACGAGT GCCTAAGTGT TTTGGTTATC AACCAGGTAA    600
GCTATGAGAA AGCCCAGCCA TAAATGGGGT TAGGTTGAAG CAAGTCTTCA TATGGTGCGA    660
CACAAGGGGT GTAGTAGGGT GTCGTCAAAC TGAAAGGTTT GATAGCTCTA AGCTTGTGCT    720
TCTGTGGGTC AAGCCTCAAG TGCTGATCTG TGGTGTCGTC TACCTGATAA CTTTCACTTT    780
TTCGAGTGAA ATTCAGGAGG CGAAACTATG GGTCAAGCCC AGCTTTGCTG GGGTTCGGCA    840
CATCCAGCTT ACAGCATTGG TGCTCTTGCG AAGCTGAAGC ACAAAAATCT AATCCAGGGT    900
TTGGGTTTTT TATACCAGAA GCAAAACAAA AAAATAAAAC AAAGAAAAAT TTTCGAGCGA    960
AAAAATATTT TGGAATTTTT TAAAGGCGAT ACTTGCTACC GCACTTTTGC CATATTTAAA   1020
ACCTGACTAT CTTTATAAGT TAATAGATAT ATCCGTTAGA TTATAAAGTA TGTTAAAAAC   1080
GAGTAAAAAC AATAACTTAT ATATTTAATT CTGAATTATA TTTGACAGTG ATTATTTAAT   1140
ATATTAAGAG ATATATCTAT TAGCTTAAAT ATAACTAAAA AAAGAGGTAA ATATATGGAT   1200
TGTGTATTTA AAAAAGCATT AGAAAATGAA ATAGAACATT ATAAAAAAGA CGGTGATATC   1260
AAATCTTTCT TACAATACTT GCATTACTTT GATATAGATA AAGCATTAAA TGGTGATGAA   1320
TGTGGCGATA TTATAAACTC AAATTTATCC ATTGATGAAA GTTTTGATCT TCTTGATGTT   1380
GAGCACAATT TCGGCTGGGC TTTCAATAAA ATAATACAGA GACGAAATGA ATATTTATCA   1440
TCAGCTAAAA CTGAAAATGA TTTTAAAAAA TACTCGTTCT TTATTCATTC GATCAATTGG   1500
GAAGAATTTA ATTACGATGA GATGAGTACA ATACATCAAG AAATGATTAA AGGATTAGAT   1560
AATTACACAT ATGGAGAAAT AACCATATGA ATAATAAAAT AAGAGAATAT ATTGATTTCG   1620
AAATAACAAA AGATATAAAA GAAAGTCAGC TCTTAAAAAT ATCTGCATTG ATCGATGTTT   1680
TAAAAGTAGA TGAAAAATTT ATTGATGAAG AGGATTTGCA ACTAAAGATA TTGAAAATAT   1740
CGTATGAAAA TCCTATTGAT GATCCAGATG ATGGCATAAG AAAATCACAA TTCGCACGAA   1800
GAAATGCCTA TGCTTTCCGC ATTAAAAAAA CAAGCAAAAA GAGATCT                 1847

          (2) INFORMATION FOR SEQ ID NO:3:

       (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 371 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asn Phe Leu His Trp Lys Phe Glu Lys Ile Arg Gln Lys Lys Leu Lys
 1               5                  10                  15

Trp Lys Lys Tyr Tyr Tyr Lys Lys Arg Arg Ser Asp Met Asp Phe Lys
            20                  25                  30

Ser Arg Lys Leu Thr Leu Asn Glu Lys Lys Asp Leu Glu Lys Ile Tyr
        35                  40                  45

Ala Glu Ser Glu Leu Lys Ala Lys Lys Leu Gly Thr Gln Pro Gly Val
    50                  55                  60

Val Leu Glu Met Thr Met Lys Glu Met Met Lys Asn Ile Asn Leu Asp
65                  70                  75                  80

Val Asn Glu Glu Thr Ala Gly Gln Tyr Arg Lys Leu Phe Lys Asn Lys
```

```
                    85                  90                  95

Val Glu His Ser Lys Ser Asp Asp Leu Val Thr Gly Leu Leu Glu Cys
            100                 105                 110

Gly Thr Arg Asn Ser Phe Asp Lys Thr Arg Ser Ala Phe Arg Phe Cys
        115                 120                 125

Ile Cys Glu Arg Ile Gln Gln Leu Arg Lys Glu Ala Asp Asn Ala Arg
    130                 135                 140

Arg Val Lys Asp Phe Asp Thr Met Lys Ala Lys Thr Lys Glu Ala Phe
145                 150                 155                 160

Glu Leu Ser Phe Val Phe Asp Lys Asp Phe Leu Ser Glu Asn Arg Ile
                165                 170                 175

Gln Trp Asn Asp Ile Ser His Asn Lys Lys Asp Ser Ala Ser Lys Arg
            180                 185                 190

Lys Thr Met Lys Glu Ala Asp Thr Met Asp Asp Ile Phe Lys Arg Leu
        195                 200                 205

Lys Asn Asn Lys Ser Thr Tyr Asp Arg Tyr Ala Gly Phe Leu Ser Ile
    210                 215                 220

Cys Ser Ile Thr Gly Cys Arg Pro Ala Glu Val Leu Lys Gly Ile Glu
225                 230                 235                 240

Ile Val Arg Asn Arg Tyr Glu Asp Gly Ile Ser Phe Lys Ile Leu Gly
                245                 250                 255
Ala Lys Val Gly Asn Asp Arg Gly Gln Ser Glu Arg Thr Leu His Phe
            260                 265                 270

Asp Leu Ser Lys Tyr His Asp Asn Glu Gln Met Asn Tyr Ile Leu Ser
        275                 280                 285

Gln Leu Lys Asp Asn Lys Phe Phe Tyr Lys Pro Asp Gly Lys Leu Tyr
    290                 295                 300

Asn Ser Leu Arg Gln Tyr Leu Tyr Ile Gln His Arg Thr Phe Ser Leu
305                 310                 315                 320

Tyr Thr Leu Arg His Arg Val Ala Ser Asp Leu Lys Ala Ser Gly Ala
                325                 330                 335

Asp Asp Phe Thr Ile Ala Ala Xaa Leu Gly His Arg Val Thr Gln Ser
            340                 345                 350

Gln Glu Leu Leu Arg Leu Cys Ser Phe Val Xaa Arg Trp Tyr Arg Cys
        355                 360                 365

Asn Trp Cys
```

206 370
207
208 1

**SEQUENCE VERIFICATION REPORT**
PATENT APPLICATION . *US/08/876,132*

DATE: 09/09/98
TIME: 15:03:10

***INPUT SET: S28494.raw***

| Line | Error | Original Text |
|---|---|---|